Amendments to the Claims:

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of Claims:

1. (Original) A method for the detection of a polymorphism in OATP8 in a human which method comprises:

(i) determining the sequence of the human at any one of the following positions:

positions 743, 811, 2021 and 2380 of SEQ ID NO: 16;

positions 233 and 256 of SEQ ID NO: 17; or

(ii) determining the sequence of the human, wherein the human is a Caucasian human, at any one of the following positions:

positions 389, 410 and 389-392 of SEQ ID NO: 15;

positions 378, 1877 and 2501-2505 of SEQ ID NO: 16;

position 112 of SEQ ID NO: 17.

2. (Original) A method according to claim 1 wherein the polymorphism is further defined as:

polymorphism at position 389 is presence of A and/or T;

polymorphism at position 410 is presence of T and/or A;

polymorphism at position 389-392 is presence of ATAT and/or TAGA;

polymorphism at position 743 is presence of A and/or G;

polymorphism at position 811 is presence of G and/or C ;

polymorphism at position 2021 is presence of G and/or A ;

polymorphism at position 2380 is presence of A and/or T;

polymorphism at position 378 is presence of G and/or T;

polymorphism at position 1877 is presence of A and/or G;

polymorphism at position 2501-2505 is presence of AAAAA and/or AAAAAA ;

polymorphism at position 233 is presence of Ile and/or Met;

polymorphism at position 256 is presence of Gly and/or Ala; and

polymorphism at position 112 is presence of Ser and/or Ala.

3. (Previously presented) A method according to claim 1 wherein the method for detection of a nucleic acid polymorphism is selected from amplification refractory mutation system and restriction fragment length polymorphism.

4. (Canceled)

5. (Original) A polynucleotide comprising at least 20 contiguous bases of the human OATP8 gene and comprising an allelic variant selected from any of the following:

Region	variant	Position
Exon 6	G	743 (SEQ ID NO: 16)
Exon 7	C	811 (SEQ ID NO: 16)
Exon 14	A	2021 (SEQ ID NO: 16)
3' UTR	T	2380 (SEQ ID NO: 16)

6. (Original) An allele specific primer capable of detecting an OATP8 gene polymorphism at one of the following positions: positions 389, 410 and 389-392 of SEQ ID NO: 15; positions 743, 811, 2021, 2380, 378, 1877 and 2501-2505 of SEQ ID NO: 16.

7. (Original) An allele specific oligonucleotide probe capable of detecting a OATP8 gene polymorphism at one of the following positions: positions 389, 410 and 289-392 of SEQ ID NO: 15; positions 743, 811, 2021, 2380, 378, 1877 and 2501-2505 of SEQ ID NO: 16.

8. (Previously presented) A diagnostic kit comprising the allele-specific primer of claim 6.

9. (Original) A method of treating a human in need of treatment with a drug transportable by OATP8 in which the method comprises detection of a polymorphism in OATP8 in a human, which method comprises:

(i) determining the sequence of the human at one of the following positions:
positions 743, 811, 2021, 2380 of SEQ ID NO: 16;

positions 233 and 256 of SEQ ID NO: 17; or

determining the sequence of the human, wherein the human is a Caucasian human, at one of the following positions:

positions 389,410 and 389-392 of SEQ ID NO: 15;

positions 378, 1877 and 2501-2505 of SEQ ID NO: 16;

position 112 of SEQ ID NO: 17; and

ii) administering an effective amount of the drug.

10. (Canceled)

11. (Original) An allelic variant of human OATP8 polypeptide comprising:

a methionine at position 233 of SEQ ID NO: 17;

an alanine at position 256 of SEQ ID NO: 17;

an alanine at position 112 of SEQ ID NO: 17;

or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 233, 256 or 112 of SEQ ID NO: 17.

12. (Original) An antibody specific for an allelic variant of human OATP8 polypeptide as described herein having:

a methionine at position 233 of SEQ ID NO: 17;

an alanine at position 256 of SEQ ID NO: 17;

an alanine at position 112 of SEQ ID NO: 17;

or a fragment thereof comprising at least 10 amino acids provided that the fragment comprises the allelic variant at position 233, 256 or 112 of SEQ ID NO: 17.

13. (Original) A diagnostic kit comprising an antibody of claim 12.

14. (Previously presented) A diagnostic kit comprising the allele specific oligonucleotide probe of claim 7.

15. (New) A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP8 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as being in need of treatment with a therapeutic agent transportable by OATP8, wherein the sample comprises a nucleotide at each of the following nucleotide positions:
positions 389, 389-392, and 410 as defined by the positions in SEQ ID NO:15; and
positions 378, 743, 811, 1877, 2021, 2380, and 2501-2505 as defined by the positions in SEQ ID NO:16; and

(b) testing the sample to determine the identity of the nucleotide at one or more of the nucleotide positions.

16. (New) The method of claim 15, comprising determining the identity of the nucleotide at position 811 of SEQ ID NO:16.

17. (New) A method for determining the presence or absence of a SNP in an OATP8 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent transportable by OATP8, wherein the sample comprises a nucleotide at each of the following nucleotide positions:
positions 389, 389-392, and 410 as defined by the positions in SEQ ID NO:15; and
positions 378, 743, 811, 1877, 2021, 2380, and 2501-2505, as defined by the positions in SEQ ID NO:16; and

(b) testing the sample to determine the identities of all 17 nucleotides.

18. (New) A method for determining the presence or absence of a SNP in an OATP8 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as in need of a drug transportable by OATP8, wherein the sample comprises a nucleotide at position 811 of the OATP8 gene as defined by the position in SEQ ID NO:16 and a nucleotide at at least one additional position selected from the group consisting of:

positions 389, 410, and 389-392 as defined by the positions in SEQ ID NO:15; and positions 378, 1877, 2501-2505, 743, 2021, and 2380 as defined by the positions in SEQ ID NO:16; and

(b) testing the sample to determine the identity of the nucleotide at one or more of the nucleotide positions.

19. (New) A method for determining the presence or absence of a single nucleotide polymorphism (SNP) in an OATP8 gene, the method comprising:

(a) providing a nucleic acid sample from a human identified as in need of treatment with a therapeutic agent transportable by OATP8, wherein the sample comprises a nucleotide at a position corresponding to position 811 of SEQ ID NO:16; and

(b) testing the sample to determine the identity of the nucleotide.

20. (New) The method of claim 19, wherein the therapeutic agent is a statin.

21. (New) The method of claim 19, wherein step (b) comprises performing a technique selected from the group consisting of an ARMS™, ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction-site based PCR, and FRET.

22. (New) The method of claim 19, further comprising:

(c) determining that the nucleotide at position 811 is not a G.

23. (New) The method of claim 19, further comprising:

(c) determining that the nucleotide at position 811 is a C.

24. (New) The method of claim 19, wherein the nucleotide is in a codon that does not encode a glycine.

25. (New) The method of claim 19, wherein the nucleotide is in a codon that encodes an alanine.

26. (New) The method of claim 19, further comprising:

(c) administering an effective amount of the therapeutic agent to the human.

27. (New) A method to assess the pharmacogenetics of a drug, the method comprising:

(a) providing a nucleic acid sample from a human, wherein the sample comprises a nucleotide at a position corresponding to position 811 of SEQ ID NO:16;

(b) determining the identity of the nucleotide; and

(c) correlating (i) the identity of the nucleotide to (ii) the human's response following administration of the drug, thereby assessing the pharmacogenetics of the drug.

28. (New) A method of treatment comprising:

(a) identifying a patient in need of treatment with a therapeutic agent transportable by OATP8;

(b) determining the identity of the nucleotide at the position corresponding to position 811 of SEQ ID NO:16 in a nucleic acid sample of the patient; and

(c) administering to the patient an effective amount of a therapeutic agent transportable by OATP8, wherein the therapeutic agent is selected according to whether the nucleotide at the position corresponding to position 811 of SEQ ID NO:1 is a G or is not a G.

29. (New) The method of claim 28, wherein step (b) comprises:

(i) providing a nucleic acid sample from the patient, wherein the sample comprises a nucleotide at a position corresponding to position 811 of SEQ ID NO:16; and

(ii) determining the identity of the nucleotide by use of a method selected from the group consisting of an ARMS™ or ALEX™ assay, COPS, Taqman™, Molecular Beacons, RFLP, restriction site based PCR or FRET.

30. (New) The method of claim 28, wherein the nucleotide is not a G.

31. (New) The method of claim 28 wherein the nucleotide is a C.